









GenCore version 5.1.3  
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M protein - protein search, using sw model

Run on: January 13, 2003, 15:56:17 : Search time 13 612 Seconds  
(without alignments)  
1604.450 Million cell updates/sec

Title: US-09-234-733a-5

Perfect score: 1118  
Sequence: 1 NQIVQGFENEDNVIQGV.....VAQVGEIRVCEALNTAQ 128

Matrix table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 281224 seqs, 3613442 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 731\*  
1: PIR1\*  
2: PIR2\*  
3: PIR3\*  
4: PIR4\*

Pired. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by integers of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match length	DB ID	Description
No matches found					

Search completed: January 13, 2003, 15:59:41  
Job time: 13.6612 secs

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CM protein - protein search, using SW model

Run on: January 13, 2003, 10:04:50, Search time 9.0046 seconds  
(without alignments)  
1180.455 Million cell updates/sec

Title: US-09-234-733a-5  
Protein score: 1118  
Sequence: 1 MDIWEYFQDNGHWISLWF ..... VAGYGEIHWLGEALNTALG 228

Scoring table: BLOSUM62  
Gapop 11.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 9  
Maximum DB seq length: 200000000

Post processing: Minimum Match 93%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt 401\*

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
No matches found						

Search completed: January 13, 2003, 15:59:05  
Job time: 8.0926 secs









JmolCore version 5.1.3  
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QM protein - protein search, using sw model

Run on: January 13, 2003, 15:57:48 : Search time 8.99174 Seconds  
(without alignments)  
\$52.360 Million cell updates/sec

Title: US-09-234 733a-2

Perfect score: 1002

Sequence: 1 MEFFRFLVITGSGIAITGFS.....VAGVGEIRFLGELNTALQ 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Query: 11974 seqs, 1940157 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 2

Maximum DB seq length: 200000000

Post processing: Minimum Match 93%

Maximum Match 100%

Listing first 45 summaries

Database: 1 Published Applications AA\*

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1: /j02_7/f1/jat11/f11a/US38_NEW_PUB.pep.*
2: /cgn2_6/f1/polar11/f11a/ECT_NEW_PUB.pep.*
3: /cgn2_6/f1/polar11/f11a/US36_NEW_PUB.pep.*
4: /cgn2_6/f1/polar11/f11a/US36_PDBOMB.pep.*
5: /cgn2_6/f1/polar11/f11a/US37_NEW_PUB.pep.*
6: /cgn2_6/f1/polar11/f11a/US37_PDBOMB.pep.*
7: /cgn2_6/f1/polar11/f11a/US38_NEW_PUB.pep.*
8: /cgn2_6/f1/polar11/f11a/US38_PDBOMB.pep.*
9: /cgn2_6/f1/polar11/f11a/US39_NEW_PUB.pep.*
10: /cgn2_6/f1/polar11/f11a/US39_PDBOMB.pep.*
11: /cgn2_6/f1/polar11/f11a/US40_NEW_PUB.pep.*
12: /cgn2_6/f1/polar11/f11a/US40_PDBOMB.pep.*
13: /cgn2_6/f1/polar11/f11a/US41_NEW_PUB.pep.*
14: /cgn2_6/f1/polar11/f11a/US41_PDBOMB.pep.*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Score	Match Length DB ID	Description
No matches found			

Search completed: January 13, 2003, 16:00:38  
Run time: 8.99174 secs

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W protein protein search, using SW model

Run on: January 13, 2003, 15:59:41, Search time 15.389 Seconds  
(without alignments)  
1604.450 Million cell updates/sec

Title: US-09-234-733a-2  
Perfect score: 1242  
Sequence: 1 MEKRYKLVYRTSSIAATTFSS.....VAQVDLIRVLDALNTALD 256

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Sequences: 29324 seqs, 9613432 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 2  
Maximum DB seq length: 20000000

Post processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 731\*  
1: PIR1\*  
2: PIR2\*  
3: PIR3\*  
4: PIR4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
No matches found					

Search completed: January 13, 2003, 15:59:41  
Job time: 16.398 secs

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SW Protein - protein search, using sw model

Run on: January 13, 2003, 15:53:12 : Search time 9.99174 Seconds  
(without alignments)  
1180.855 Million cell updates/sec

Title: US-09-234-733A.2

Perfect score: 1252  
Sequence: 1 MFPRHLYLTLASLALILTS.....VWVQLEIRVLEVALIALQ 256

Scoring matrix: BLOSUM62  
Gapop 10.0, Gapext 0.5

Sequidbed: 112802 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 0

Minimum ES seq length: 5  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_401\*

Note: No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by re-sampling of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
No matches found					

Search completed: January 13, 2003, 15:58:05  
Job time: 9.99174 secs